

# **ESC-113**

# **TERM**

# **PROJECT**

**Presented by Group-3**

# OVERVIEW

- Introduction
- Michaelis-Menten
- Model-History
- Importance of the model
- Mathematical Model
- MATLAB Implementation
- How the model works?
- Similar Models
- Reference

# INTRODUCTION

- The Michaelis-Menten equation is a fundamental model in enzyme kinetics that quantitatively describes how the reaction rate varies with substrate concentration. Developed by Leonor Michaelis and Maud Menten, this model was initially applied to the enzyme invertase, which catalyzes the hydrolysis of sugars. It remains a cornerstone in biochemistry and pharmacology for analyzing enzymatic reaction dynamics.
- In this project, we have developed a MATLAB-based model that takes enzyme parameters as input and uses the Michaelis-Menten equation to simulate the reaction kinetics.

## ADDITIONAL NOTES:

- A user-friendly MATLAB GUI has been created to allow easy input of parameters and real-time visualization of results. The numerical solution is computed using the Runge-Kutta 4th Order (RK4) method, ensuring high accuracy and stability in simulating the system's behavior over time.

# IMPORTANCE OF THE MODEL

The Michaelis-Menten model is a cornerstone of enzyme kinetics, offering a simplified yet powerful framework to understand how enzymes interact with substrates. Its importance lies in the ability to:

**Quantitatively analyze enzymatic reactions**, enabling researchers to determine critical parameters like maximum reaction rate  $V_{max}$  and substrate affinity  $K_m$ .

**Predict the effect of substrate concentration on reaction velocity**, which is crucial in designing biochemical experiments and interpreting lab results.

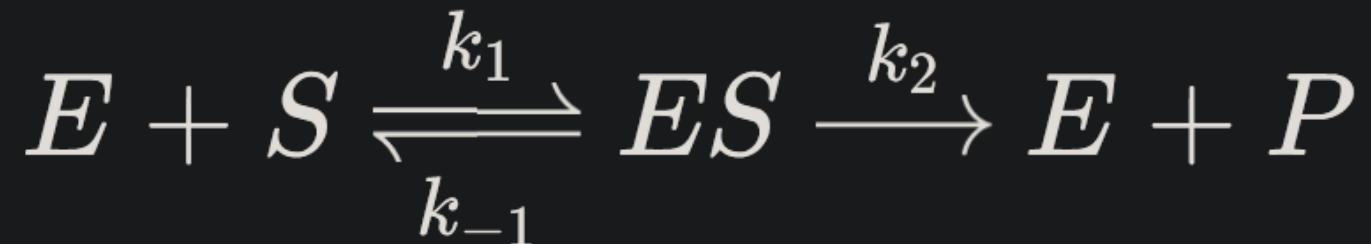
**Aid drug development and pharmacology**, where understanding how drugs (inhibitors) affect enzyme activity helps in optimizing dosages and minimizing side effects.

**Model metabolic pathways in systems biology**, providing insight into how enzymes regulate biological processes under different conditions.

**By simplifying complex biochemical interactions into manageable equations, the Michaelis-Menten model has become an essential tool across biochemistry, molecular biology, and medicine.**

# REACTION MECHANISM BEHIND THE MICHAELIS-MENTEN MODEL

The Michaelis-Menten model is based on a simple enzymatic reaction that proceeds through the following steps:

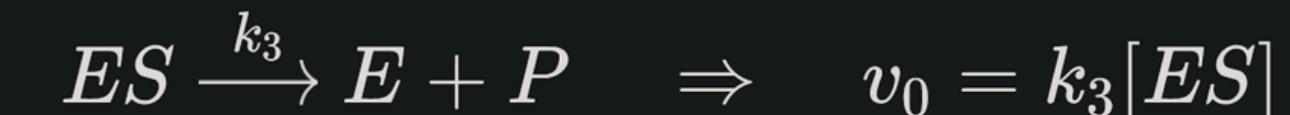


<b>E :</b>	Free enzyme	<b>k<sub>1</sub>:</b>	Rate constant for enzyme-substrate binding
<b>S :</b>	Substrate		
<b>ES :</b>	Enzyme-substrate complex	<b>k<sub>-1</sub>:</b>	Rate constant for complex dissociation
<b>P :</b>	Product	<b>k<sub>2</sub>:</b>	Rate constant for product formation



The enzyme interacts with the substrate by binding to its active site to form the enzyme-substrate complex, ES. That reaction is followed by the decomposition of ES to regenerate the free enzyme,

E, and the new product, P.



# MATHEMATICAL MODEL

The Michaelis-Menten equation, which describes the reaction rate, is given by:

$$v = \frac{V_{\max}[S]}{K_m + [S]}$$

The ES complex is formed by combining enzyme E with substrate S at rate constant  $k_1$ . The ES complex can either dissociate to form EF (free enzyme) and S, or form product P at rate constant  $k_2$  and  $k_3$ , respectively.

The velocity equation can be derived using the steady state

- $v$  = rate of reaction =  $-d[S]/dt$
- $[S]$  = substrate concentration
- $V_{\max}$  =  $k_2E_0$  (maximum reaction velocity, depends on enzyme concentration)
- $K_M$  =  $(k_{-1}+k_2)/k_1$  (Michaelis constant, indicating enzyme efficiency)
- $E_0$  = enzyme concentration

approximation:

$$\frac{d[ES]}{dt} = k_1[E][S] + k_2[ES] + k_3[ES] = 0$$

# DESIGNING MODEL IN MATLAB

## Implementing RK-4 Algorithm

$$y_{i+1} = y_i + \frac{h}{6} (k_1 + 2k_2 + 2k_3 + k_4)$$

$$k_1 = f(x_i, y_i)$$

$$k_2 = f\left(x_i + \frac{h}{2}, y_i + \frac{h}{2}k_1\right)$$

$$k_3 = f\left(x_i + \frac{h}{2}, y_i + \frac{h}{2}k_2\right)$$

$$k_4 = f(x_i + h, y_i + hk_3)$$

## Using Built-in GUI

We developed an interactive MATLAB app using built-in GUI components that enables users to:

- **Input Parameters:** Easily enter values like  $V_{max}$ ,  $K_m$ , and initial substrate concentration.
- **Run Simulations:** Execute the RK-4 solver with a single click.
- **Visualize Results:** View dynamic plots that update as parameters change.

This streamlined interface makes modeling accessible to users of all levels, eliminating the need for manual scripting.

# Applications and examples in MATLAB for some specific enzymes

Chymotrypsin

 $1.5 \times 10^{-2}$ 

0.14

9.3

Initial Substrate ( $S_0$ ):

0.1

Enzyme Concentration ( $E_0$ ):

1

Michaelis Constant ( $K_M$ ):

0.015

Catalytic Constant ( $k_2$ ):

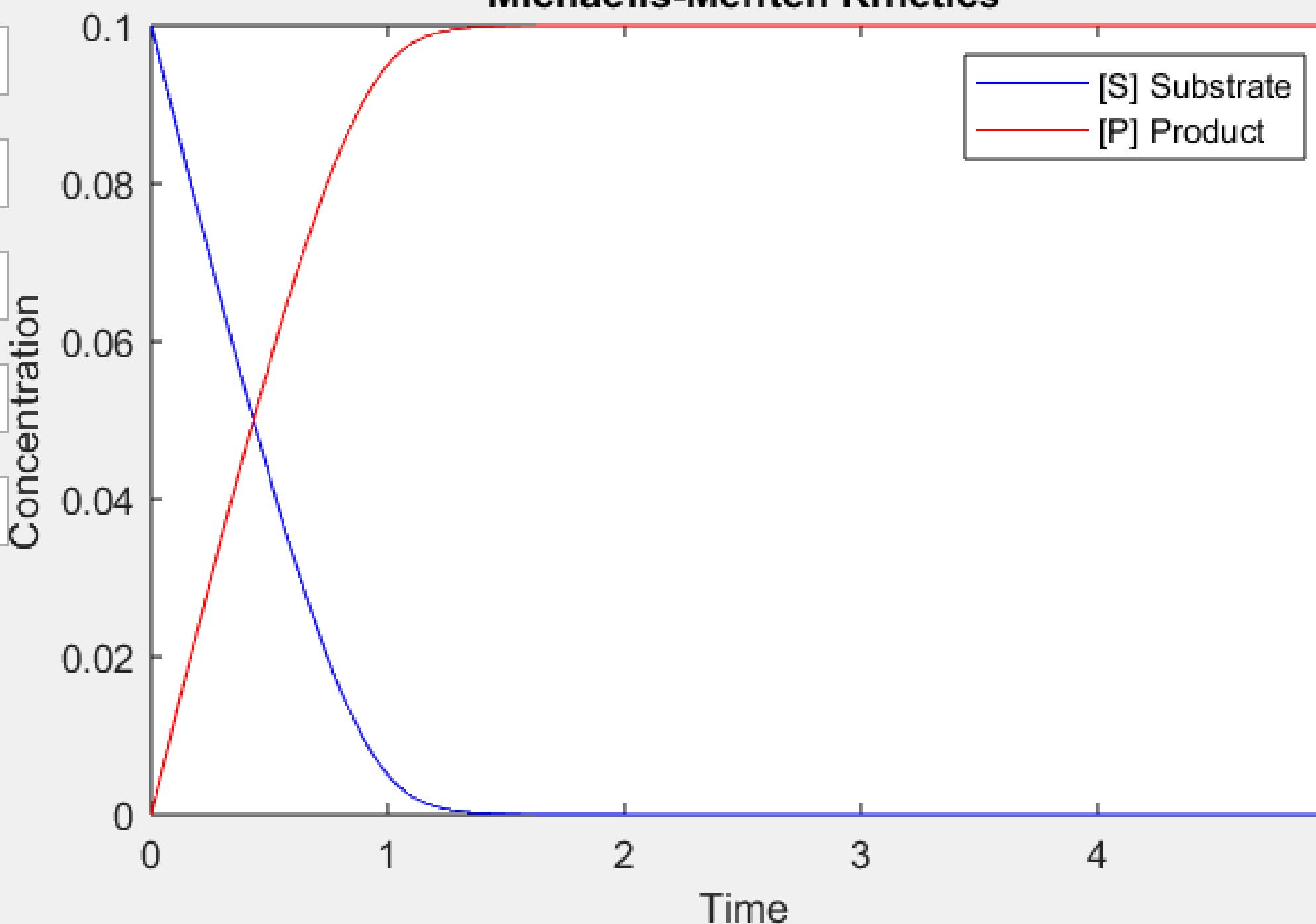
0.14

Simulation Time ( $t_{max}$ ):

5

Run Simulation

## Michaelis-Menten Kinetics



Pepsin

$3.0 \times 10^{-4}$

0.50

$1.7 \times 10^3$

Initial Substrate ( $S_0$ ):

50

Enzyme Concentration ( $E_0$ ):

1

Michaelis Constant ( $K_M$ ):

0.0003

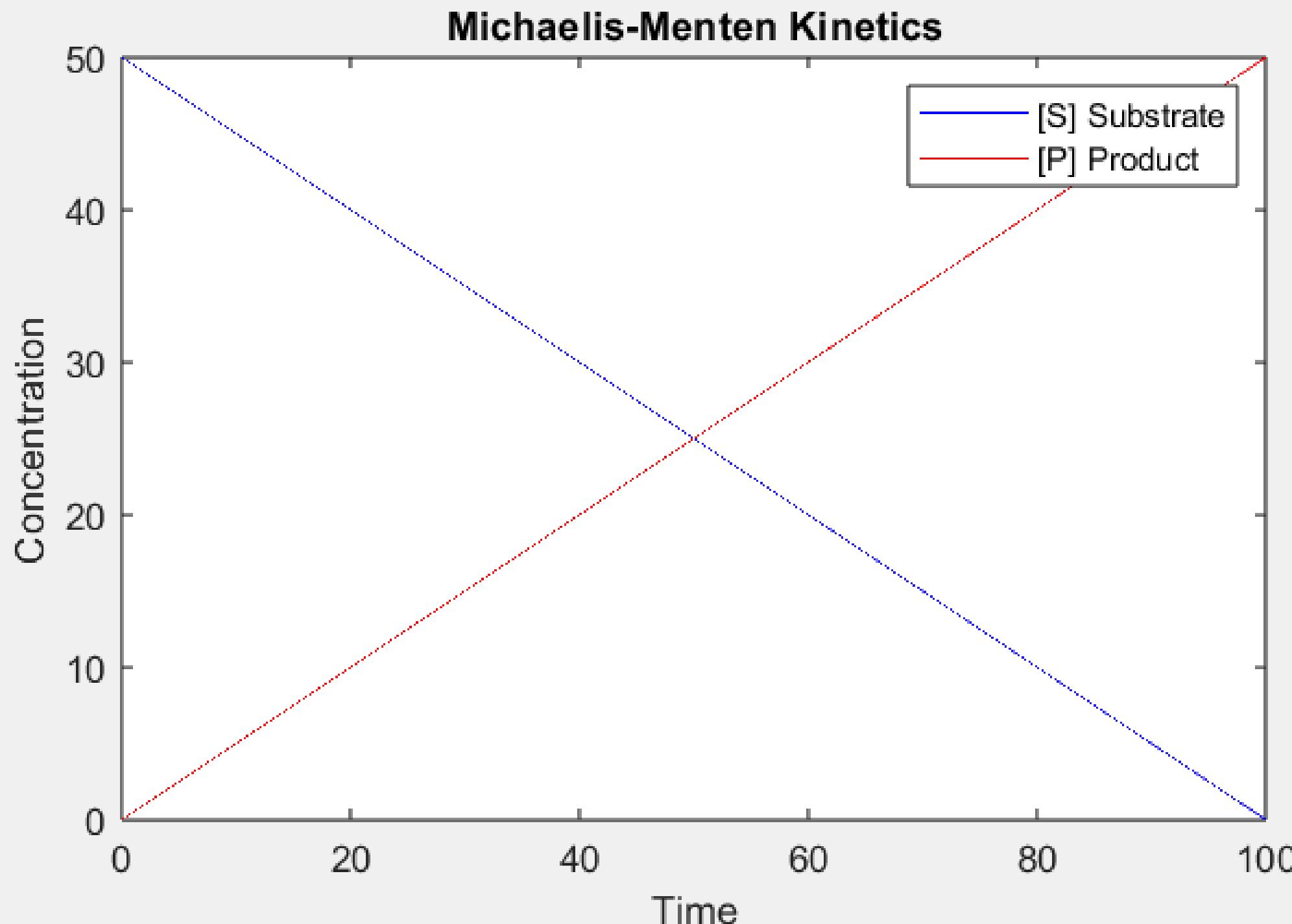
Catalytic Constant ( $k_2$ ):

0.5

Simulation Time ( $t_{max}$ ):

100

Run Simulation



tRNA synthetase

$9.0 \times 10^{-4}$

7.6

$8.4 \times 10^3$

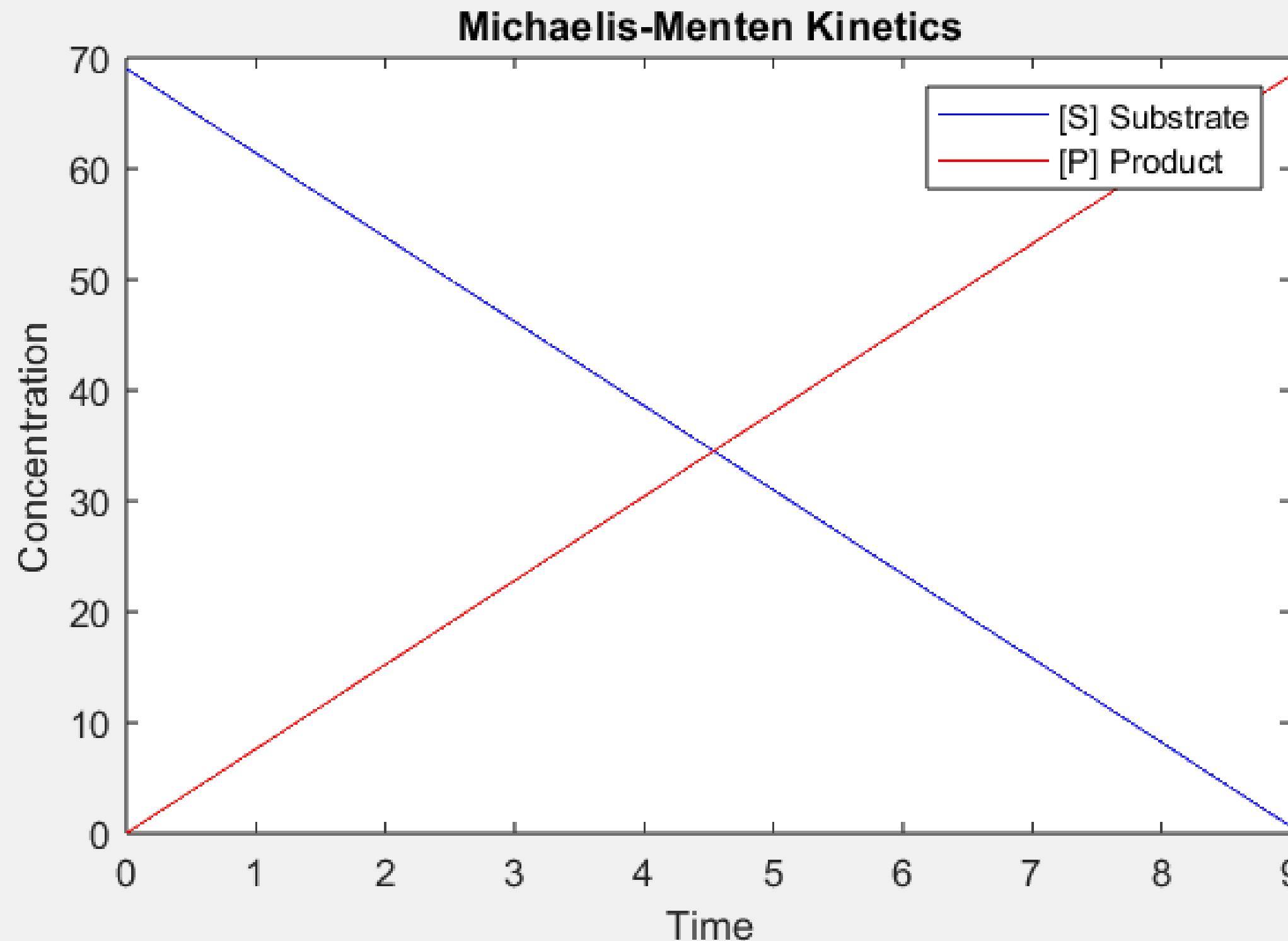
Initial Substrate ( $S_0$ ):

Enzyme Concentration ( $E_0$ ):

Michaelis Constant ( $K_M$ ):

Catalytic Constant ( $k_2$ ):

Simulation Time ( $t_{max}$ ):



# EXTENSIONS OF THE MICHAELIS-MENTEN FRAMEWORK

## 1. Competitive Inhibition

- **What it is:** An inhibitor competes with the substrate to bind to the enzyme.
- **Relation to Michaelis-Menten:** Similar structure but changes the effective  $K_m$  (you need more substrate to reach the same rate).
- **Why RK4 works:** You get slightly more complex differential equations, but RK4 can still solve them easily.

## 3. Uncompetitive Inhibition

- **What it is:** Inhibitor binds only after the enzyme binds to the substrate.
- **Relation to MM model:** Both  $K_m$  and  $V_{max}$  get reduced.
- **Why RK4 works:** Again, you just solve updated equations—RK4 fits perfectly here too.

## 2. Non-Competitive Inhibition

- **What it is:** Inhibitor binds to the enzyme at a different site (not the active site), slowing down the reaction.
- **Relation to Michaelis-Menten:** Lowers the maximum reaction rate ( $V_{max}$ ) but  $K_m$  stays the same.
- **RK4 usage:** Still a set of ODEs—RK4 can handle this without any problem.

## 4. Substrate Inhibition

- **What it is:** Too much substrate actually slows the enzyme down.
- **Relation to MM model:** Adds a new term to the equation to reduce rate at high substrate levels.
- **Why RK4:** The extra term just adds complexity, which RK4 handles well.

# CONCLUSION

- In this project, we successfully developed a MATLAB-based model to simulate enzyme kinetics using the Michaelis-Menten equation. By leveraging a user-friendly GUI, we streamlined the process, enabling users to effortlessly input key parameters, run simulations via a robust RK-4 solver, and visualize dynamic results in real time.
- This approach not only enhances accessibility for users at various experience levels but also improves the efficiency and accuracy of enzymatic reaction analyses. Ultimately, the integration of computational modeling with interactive visualization provides a valuable tool for both educational and research applications in biochemistry and pharmacology.
- Future enhancements could include incorporating additional kinetic models, optimizing numerical methods, and expanding the GUI features for broader usability, further solidifying the role of computational methods in advancing our understanding of biochemical processes.

# REFERENCE

**Link:** <https://www.sciencedirect.com/topics/engineering/michaelis-menten-equation#:~:text=2.1%20Michaelis%2DMenten%20Model&text=The%20rate%20constants%20are%20represented,the%20quasi%20steady%2Dstate%20assumption.>

**Brief Description:** About the Michaelis-Menten Equation

**Link:** [https://chem.libretexts.org/Bookshelves/Biological\\_Chemistry/Supplemental\\_Modules\\_\(Biological\\_Chemistry\)/Enzymes/Enzymatic\\_Kinetics/Michaelis-Menten\\_Kinetics](https://chem.libretexts.org/Bookshelves/Biological_Chemistry/Supplemental_Modules_(Biological_Chemistry)/Enzymes/Enzymatic_Kinetics/Michaelis-Menten_Kinetics)

**Brief Description:** Derivation of the Michaelis-Menten Equation

**Link:** <https://www.wikipedia.org/>

**Brief Description:** For taking the constant parameters of the enzymes

# Thank You

Made By-

Prathmesh Thorat  
Kshitij Jain  
Rohan Upadhyay  
Falgun Dadhich  
Mayur Pachpute

Madhur Kumar  
Thamesh Patra  
Priyanshu  
Krish Mundhra  
Dev Kushwaha